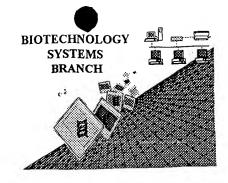# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/508,658_

Source: _/655_

Date Processed by STIC: _6/21/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE ERRORED SEQUENCE LISTINGS, PLEASE** USE THE **CHECKER VERSION 3.0 PROGRAM,** ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/508,658

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos · The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)_____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____Skipped Sequences (OLD RULES) Sequence(s)_____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences (NEW RULES) Sequence(s)_____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____Use of <220> Sequence(s) 1 - end of file missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

1655

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/508,658

DATE: 06/21/2001
TIME: 11:43:24

Input Set : A:\U0126539.app
Output Set: N:\CRF3\06202001\I508658.raw

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 3 <110> APPLICANT: Krohn, Kai
 4        Heino, Maarit
 5        Peterson, Part
 6        Scott S., Hamish
 7        Antonarakis E., Stylianos
 8        Lalioti D., Maria
 9        Shimizu, Nobuyoshi
10        Kudoh, Jun
12 <120> TITLE OF INVENTION: NOVEL GENE DEFECTIVE IN APECED AND ITS USE
14 <130> FILE REFERENCE: U0126539
16 <140> CURRENT APPLICATION NUMBER: 09/508,658
17 <141> CURRENT FILING DATE: 2000-11-03
19 <150> PRIOR APPLICATION NUMBER: PCT/FI98/00749
20 <151> PRIOR FILING DATE: 1998-09-23
22 <150> PRIOR APPLICATION NUMBER: 973762
23 <151> PRIOR FILING DATE: 1997-09-23
25 <160> NUMBER OF SEQ ID NOS: 36
27 <170> SOFTWARE: PatentIn Ver. 2.0
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 2036
31 <212> TYPE: DNA
32 <213> ORGANISM: Homo sapiens
34 <220> FEATURE:
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36 <222> LOCATION: (137)..(1774)
37 <223> OTHER INFORMATION: /product="AIR-1"
39 <220> FEATURE:
40 <221> NAME/KEY: mat_peptide
41 <222> LOCATION: (1)..(545)
42 <223> OTHER INFORMATION: /product="AIR-1"
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47 cgaggccaag cgagggctg ccagtgtccc gggacccacc gcgtccgccc cagccccggg 120
49 tccccgcgcc caccc atg gcg acg gac gcg gcg cta cgc cgg ctt ctg agg 172
50              Met Ala Thr Asp Ala Ala Leu Arg Arg Leu Leu Arg
51              1            5              10
53 ctg cac cgc acg gag atc gcg gtg gcc gtg gac agc gcc ttc cca ctg 220
54 Leu His Arg Thr Glu Ile Ala Val Ala Val Asp Ser Ala Phe Pro Leu
55       15           20           25
57 ctg cac gcg ctg gct gac cac gac gtg gtc ccc gag gac aag ttt cag 268
58 Leu His Ala Leu Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln
59       30           35           40
61 gag acg ctt cat ctg aag gaa aag gag ggc tgc ccc cag gcc ttc cac 316
62 Glu Thr Leu His Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His
63    45           50           55           60
65 gcc ctc ctg tcc tgg ctg ctg acc cag gac tcc aca gcc atc ctg gac 364
66 Ala Leu Leu Ser Trp Leu Leu Thr Gln Asp Ser Thr Ala Ile Leu Asp
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RAW SEQUENCE LISTING   DATE: 06/21/2001
PATENT APPLICATION: US/09/508,658   TIME: 11:43:24

Input Set : A:\U0126539.app
Output Set: N:\CRF3\06202001\I508658.raw

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67              65                70                75
69 ttc tgg agg gtg ctg ttc aag gac tac aac ctg gag cgc tat ggc cgg   412
70 Phe Trp Arg Val Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Gly Arg
71          80                85                90
73 ctg cag ccc atc ctg gac agc ttc ccc aaa gat gtg gac ctc agc cag   460
74 Leu Gln Pro Ile Leu Asp Ser Phe Pro Lys Asp Val Asp Leu Ser Gln
75          95                100               105
77 ccc cgg aag ggg agg aag ccc ccg gcc gtc ccc aag gct ttg gta ccg   508
78 Pro Arg Lys Gly Arg Lys Pro Pro Ala Val Pro Lys Ala Leu Val Pro
79     110               115               120
81 cca ccc aga ctc ccc acc aag agg aag gcc tca gaa gag gct cga gct   556
82 Pro Pro Arg Leu Pro Thr Lys Arg Lys Ala Ser Glu Glu Ala Arg Ala
83 125               130               135               140
85 gcc gcg cca gca gcc ctg act cca agg ggc acc gcc agc cca ggc tct   604
86 Ala Ala Pro Ala Ala Leu Thr Pro Arg Gly Thr Ala Ser Pro Gly Ser
87               145               150               155
89 caa ctg aag gcc aag ccc ccc aag aag ccg gag agc agc gca gag cag   652
90 Gln Leu Lys Ala Lys Pro Pro Lys Lys Pro Glu Ser Ser Ala Glu Gln
91          160               165               170
93 cag cgc ctt cca ctc ggg aac ggg att cag acc atg tca gct tca gtc   700
94 Gln Arg Leu Pro Leu Gly Asn Gly Ile Gln Thr Met Ser Ala Ser Val
95          175               180               185
97 cag aga gct gtg gcc atg tcc tcc ggg gac gtc ccg gga gcc cga ggg   748
98 Gln Arg Ala Val Ala Met Ser Ser Gly Asp Val Pro Gly Ala Arg Gly
99     190               195               200
101 gcc gtg gag ggg atc ctc atc cag cag gtg ttt gag tca ggc ggc tcc   796
102 Ala Val Glu Gly Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Gly Ser
103 205               210               215               220
105 aag aag tgc atc cag gtt ggc ggg gag ttc tac act ccc agc aag ttc   844
106 Lys Lys Cys Ile Gln Val Gly Gly Glu Phe Tyr Thr Pro Ser Lys Phe
107               225               230               235
109 gaa gac tcc ggc agt ggg aag aac aag gcc cgc agc agc agt ggc ccg   892
110 Glu Asp Ser Gly Ser Gly Lys Asn Lys Ala Arg Ser Ser Ser Gly Pro
111               240               245               250
113 aag cct ctg gtt cga gcc aag gga gcc cag ggc gct gcc ccc ggt gga   940
114 Lys Pro Leu Val Arg Ala Lys Gly Ala Gln Gly Ala Ala Pro Gly Gly
115          255               260               265
117 ggt gag gct agg ctg ggc cag cag ggc agc gtt ccc gcc cct ctg gcc   988
118 Gly Glu Ala Arg Leu Gly Gln Gln Gly Ser Val Pro Ala Pro Leu Ala
119     270               275               280
121 ctc ccc agt gac ccc cag ctc cac cag aag aat gag gac gag tgt gcc   1036
122 Leu Pro Ser Asp Pro Gln Leu His Gln Lys Asn Glu Asp Glu Cys Ala
123 285               290               295               300
125 gtg tgt cgg gac ggc ggg gag ctc atc tgc tgt gac ggc tgc cct cgg   1084
126 Val Cys Arg Asp Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg
127               305               310               315
129 gcc ttc cac ctg gcc tgc ctg tcc cct ccg ctc cgg gag atc ccc agt   1132
130 Ala Phe His Leu Ala Cys Leu Ser Pro Pro Leu Arg Glu Ile Pro Ser
131               320               325               330
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RAW SEQUENCE LISTING   DATE: 06/21/2001
PATENT APPLICATION: US/09/508,658   TIME: 11:43:24

Input Set : A:\U0126539.app
Output Set: N:\CRF3\06202001\I508658.raw

```
133 ggg acc tgg agg tgc tcc agc tgc ctg cag gca aca gtc cag gag gtg   1180
134 Gly Thr Trp Arg Cys Ser Ser Cys Leu Gln Ala Thr Val Gln Glu Val
135         335                 340                 345
137 cag ccc cgg gca gag gag ccc cgg ccc cag gag cca ccc gtg gag acc   1228
138 Gln Pro Arg Ala Glu Glu Pro Arg Pro Gln Glu Pro Pro Val Glu Thr
139     350                 355                 360
141 ccg ctc ccc ccg ggg ctt agg tcg gcg gga gag gag gta aga ggt cca   1276
142 Pro Leu Pro Pro Gly Leu Arg Ser Ala Gly Glu Glu Val Arg Gly Pro
143 365                 370                 375                 380
145 cct ggg gaa ccc cta gcc ggc atg gac acg act ctt gtc tac aag cac   1324
146 Pro Gly Glu Pro Leu Ala Gly Met Asp Thr Thr Leu Val Tyr Lys His
147                 385                 390                 395
149 ctg ccg gct ccg cct tct gca gcc ccg ctg cca ggg ctg gac tcc tcg   1372
150 Leu Pro Ala Pro Pro Ser Ala Ala Pro Leu Pro Gly Leu Asp Ser Ser
151         400                 405                 410
153 gcc ctg cac ccc cta ctg tgt gtg gct cct gag ggt cag cag aac ctg   1420
154 Ala Leu His Pro Leu Leu Cys Val Ala Pro Glu Gly Gln Gln Asn Leu
155         415                 420                 425
157 gct cct ggt gcg cgt tgc ggg gtg tgc gga gat ggt acg gac gtg ctg   1468
158 Ala Pro Gly Ala Arg Cys Gly Val Cys Gly Asp Gly Thr Asp Val Leu
159     430                 435                 440
161 cgg tgt act cac tgc gcc gct gcc ttc cac tgg cgc tgc cac ttc cca   1516
162 Arg Cys Thr His Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro
163 445                 450                 455                 460
165 gcc ggc acc tcc cgg ccc ggg acg ggc ctg cgc tgc aga tcc tgc tca   1564
166 Ala Gly Thr Ser Arg Pro Gly Thr Gly Leu Arg Cys Arg Ser Cys Ser
167                 465                 470                 475
169 gga gac gtg acc cca gcc cct gtg gag ggg gtg ctg gcc ccc agc ccc   1612
170 Gly Asp Val Thr Pro Ala Pro Val Glu Gly Val Leu Ala Pro Ser Pro
171         480                 485                 490
173 gcc cgc ctg gcc cct ggg cct gcc aag gat gac act gcc agt cac gag   1660
174 Ala Arg Leu Ala Pro Gly Pro Ala Lys Asp Asp Thr Ala Ser His Glu
175         495                 500                 505
177 ccc gct ctg cac agg gat gac ctg gag tcc ctt ctg agc gag cac acc   1708
178 Pro Ala Leu His Arg Asp Asp Leu Glu Ser Leu Leu Ser Glu His Thr
179     510                 515                 520
181 ttc gat ggc atc ctg cag tgg gcc atc cag agc atg gcc cgt ccg gcg   1756
182 Phe Asp Gly Ile Leu Gln Trp Ala Ile Gln Ser Met Ala Arg Pro Ala
183 525                 530                 535                 540
185 gcc ccc ttc ccc tcc tga ccccagatgg ccgggacatg cagctctgat          1804
186 Ala Pro Phe Pro Ser
187                 545
189 gagagagtgc tgagaaggac acctccttcc tcagtcctgg aagccggccg gctgggatca 1864
191 agaaggggac agcgccacct cttgtcagtg ctcggctgta aacagctctg tgtttctggg 1924
193 gacaccagcc atcatgtgcc tggaaattaa accctgcccc acttctctac tctggaagtc 1984
195 cccgggagcc tctccttgcc tggtgaccta ctaaaaatat aaaaattagc tg          2036
198 <210> SEQ ID NO: 2
199 <211> LENGTH: 545
200 <212> TYPE: PRT
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201 <213> ORGANISM: Homo sapiens
203 <400> SEQUENCE: 2
204 Met Ala Thr Asp Ala Ala Leu Arg Arg Leu Leu Arg Leu His Arg Thr
205  1               5                  10                  15
207 Glu Ile Ala Val Ala Val Asp Ser Ala Phe Pro Leu Leu His Ala Leu
208              20                  25                  30
210 Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu His
211          35                  40                  45
213 Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu Ser
214      50                  55                  60
216 Trp Leu Leu Thr Gln Asp Ser Thr Ala Ile Leu Asp Phe Trp Arg Val
217  65                  70                  75                  80
219 Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Gly Arg Leu Gln Pro Ile
220                  85                  90                  95
222 Leu Asp Ser Phe Pro Lys Asp Val Asp Leu Ser Gln Pro Arg Lys Gly
223              100                 105                 110
225 Arg Lys Pro Pro Ala Val Pro Lys Ala Leu Val Pro Pro Pro Arg Leu
226          115                 120                 125
228 Pro Thr Lys Arg Lys Ala Ser Glu Glu Ala Arg Ala Ala Ala Pro Ala
229      130                 135                 140
231 Ala Leu Thr Pro Arg Gly Thr Ala Ser Pro Gly Ser Gln Leu Lys Ala
232 145                 150                 155                 160
234 Lys Pro Pro Lys Lys Pro Glu Ser Ser Ala Glu Gln Gln Arg Leu Pro
235              165                 170                 175
237 Leu Gly Asn Gly Ile Gln Thr Met Ser Ala Ser Val Gln Arg Ala Val
238              180                 185                 190
240 Ala Met Ser Ser Gly Asp Val Pro Gly Ala Arg Gly Ala Val Glu Gly
241          195                 200                 205
243 Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Gly Ser Lys Lys Cys Ile
244      210                 215                 220
246 Gln Val Gly Gly Glu Phe Tyr Thr Pro Ser Lys Phe Glu Asp Ser Gly
247 225                 230                 235                 240
249 Ser Gly Lys Asn Lys Ala Arg Ser Ser Ser Gly Pro Lys Pro Leu Val
250              245                 250                 255
252 Arg Ala Lys Gly Ala Gln Gly Ala Ala Pro Gly Gly Gly Glu Ala Arg
253              260                 265                 270
255 Leu Gly Gln Gln Gly Ser Val Pro Ala Pro Leu Ala Leu Pro Ser Asp
256          275                 280                 285
258 Pro Gln Leu His Gln Lys Asn Glu Asp Glu Cys Ala Val Cys Arg Asp
259      290                 295                 300
261 Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe His Leu
262 305                 310                 315                 320
264 Ala Cys Leu Ser Pro Pro Leu Arg Glu Ile Pro Ser Gly Thr Trp Arg
265              325                 330                 335
267 Cys Ser Ser Cys Leu Gln Ala Thr Val Gln Glu Val Gln Pro Arg Ala
268              340                 345                 350
270 Glu Glu Pro Arg Pro Gln Glu Pro Pro Val Glu Thr Pro Leu Pro Pro
271          355                 360                 365
273 Gly Leu Arg Ser Ala Gly Glu Glu Val Arg Gly Pro Pro Gly Glu Pro
```

Input Set : A:\U0126539.app
Output Set: N:\CRF3\06202001\I508658.raw

```
274      370                   375                 380
276 Leu Ala Gly Met Asp Thr Thr Leu Val Tyr Lys His Leu Pro Ala Pro
277 385                   390                 395                 400
279 Pro Ser Ala Ala Pro Leu Pro Gly Leu Asp Ser Ser Ala Leu His Pro
280               405               410               415
282 Leu Leu Cys Val Ala Pro Glu Gly Gln Gln Asn Leu Ala Pro Gly Ala
283               420               425               430
285 Arg Cys Gly Val Cys Gly Asp Gly Thr Asp Val Leu Arg Cys Thr His
286           435               440               445
288 Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Ala Gly Thr Ser
289     450               455               460
291 Arg Pro Gly Thr Gly Leu Arg Cys Arg Ser Cys Ser Gly Asp Val Thr
292 465               470               475               480
294 Pro Ala Pro Val Glu Gly Val Leu Ala Pro Ser Pro Ala Arg Leu Ala
295               485               490               495
297 Pro Gly Pro Ala Lys Asp Asp Thr Ala Ser His Glu Pro Ala Leu His
298           500               505               510
300 Arg Asp Asp Leu Glu Ser Leu Leu Ser Glu His Thr Phe Asp Gly Ile
301           515               520               525
303 Leu Gln Trp Ala Ile Gln Ser Met Ala Arg Pro Ala Ala Pro Phe Pro
304       530               535               540
306 Ser
307 545
310 <210> SEQ ID NO: 3
311 <211> LENGTH: 1545
312 <212> TYPE: DNA
313 <213> ORGANISM: Homo sapiens
315 <220> FEATURE:
316 <221> NAME/KEY: CDS
317 <222> LOCATION: (237)..(1283)
318 <223> OTHER INFORMATION: /product="AIR-2"
320 <220> FEATURE:
321 <221> NAME/KEY: mat_peptide
322 <222> LOCATION: (1)..(348)
323 <223> OTHER INFORMATION: /product="AIR-2"
325 <400> SEQUENCE: 3
326 agagaaagtg aggtcttctc aggctcttaa gagcatggcg tttggtccag gctgtacccg 60
328 ctgctctcag ctgggcccgt gggtgggccg ggcgcccctg ctatagccag gaggtcaagg 120
330 atccactggg aatgccatgc tcatctttcg tccccagcat ggtttcttaa tggggtagaa 180
332 gcaggtcggg agagacctcc ctgggcctgg ccccactgcc ctgtgaggaa gggttc atg 239
333                                                              Met
334                                                              1
336 tgg ttg gtg tac agt tcc ggg gcc cct gga acg cag cag cct gca aga    287
337 Trp Leu Val Tyr Ser Ser Gly Ala Pro Gly Thr Gln Gln Pro Ala Arg
338           5                   10                  15
340 aac cgg gtt ttc ttc cca ata ggg atg gcc ccg ggg ggt gtc tgt tcg    335
341 Asn Arg Val Phe Phe Pro Ile Gly Met Ala Pro Gly Gly Val Cys Ser
342           20                  25                  30
344 aga cca gat gga tgg gga aca ggt ggt cag ggc aga att tca ggc cct    383
```

```
<210> 7
<211> 20
<212> DNA
<213> Artificial Sequence
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See item 11 on Errn Summary Sheet

```
<400> 7
gatgacactg ccagtcacga                                    20
```

```
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<211> 22
<212> DNA
<213> Artificial Sequence
```

```
<400> 8
gttcccgagt ggaaggcgct gc                                 22
```

```
<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence
```

```
<400> 9
aggggacagg caggccaggt                                    20
```

The above sequences are samples of global error,

The types of errors shown exist <u>throughout</u> the Sequence Listing. Please check subsequent sequences for similar errors.

Input Set : **A:\U0126539.app**
Output Set: **N:\CRF3\06202001\I508658.raw**

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L:675 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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L:684 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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L:693 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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L:720 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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Input Set : **A:\U0126539.app**
Output Set: **N:\CRF3\06202001\I508658.raw**

L:923 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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L:932 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: